Changes made:

* visualizing results in a table for diseasesRelatedToGene and genesRelatedToDiseases
* Sorting their results and adding both nomenclature at the table (ex: both disease\_name and diseaseid)
* In the diseasesRelatedToGene I added a statement in part2 to capitalize each letter of the disease\_name because the sort function distinguish between uppercase and lower case, thus we would have had at the end like 5-6 diseases out of place because they were lowercase
* the navigation bar at the top now stays fixed in place even if you scroll down
* added a table also for the evidences in literature for both genes and diseases, added the columns nsentence and pmid to let the user find the original publication
* Fixed some sentences
* Removed correlation10 and correlationAll
* Added only one correlation which defaults to 10 rows, but allows you to customize both the number of rows and the minimum number of occurrences each rows needs. It prints the results in a table
* Modified buttons in the input
* Changed some sentences
* Organized the code of the style of the tables
* Made all the function justified-center
* Fixed the top navigation bar which was grey when the cursor hovered over it in the webpage where you can browse the tables
* Cleaned the styles in the webpages of the datatables
* Added the link to pmid links in Gene evidences and Disease Evidences
* In the distinct diseases I added a statement in part2 to capitalize each letter of the disease\_name because the sort function distinguish between uppercase and lower case, thus we would have had at the end some diseases out of place because they were lowercase
* **Massively improved correlation function. I corrected the function I wrote which was wrong and gave incorrect results, now it’s correct, it’s 20 times faster, and has a much cleaner code**